

FIGURE 1A

Map of a First IL-17 Receptor Like cDNA (SEQ ID No: 1)  
and Amino Acid (SEQ ID NO: 2)

#5

1 ATAAAAGCGCAGCGTGC GGGTGGCCTGGATCCCGCGCAGTGGCCCCGGCGATGTCGCTCGT 60  
M S L V -  
61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120  
L L S L A A L C R S A V P R E P T V Q C -  
121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGA 180  
G S E T G P S P E W M L Q H D L I P G D -  
181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGACTATTCAAT 240  
L R D L R V E P V T T S V A T G D Y S I -  
241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGTAAGGCCAC 300  
L M N V S W V L R A D A S I R L L K A T -  
301 CAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTA 360  
K I C V T G K S N F Q S Y S C V R C N Y -  
361 CACAGAGGCCTTCCAGACTCAGACCAGACCCCTCTGGTGGTAAATGGACATTTTCTACAT 420  
T E A F Q T Q T R P S G G K W T F S Y I -  
421 CGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGC 480  
G F P V E L N T V Y F I G A H N I P N A -  
481 AAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGA 540  
N M N E D G P S M S V N F T S P G C L D -  
541 CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACAT 600  
H I M K Y K K K C V K A G S L W D P N I -  
601 CACTGCTTGTGAAGAAGAATGAGGAGACAGTAGAAGTGAACCTTCACAACCACTCCCCTGGG 660  
T A C K K N E E T V E V N F T T T P L G -  
661 AAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGA 720  
N R Y M A L I Q H S T I I G F S Q V F E -  
721 GCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGAAGTGGGATACTGA 780  
P H Q K K Q T R A S V V I P V T G D S E -  
781 AGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACA 840  
G A T V Q L T P Y F P T C G S D C I R H -  
841 TAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAA 900  
K G T V V L C P Q T G V P F P L D N N K -  
901 AAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCTGCTGTCTCTGCTGGTGGCCACATGGGT 960  
S K P G G W L P L L L L S L L V A T W V -

Figure 1B

961 GCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTC 1020  
L V A G I Y L M W R H E R I K K T S F S -

1021 TACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTT 1080  
T T T L L P P I K V L V V Y P S E I C F -

1081 CCATCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCAT 1140  
H H T I C Y F T E F L Q N H C R S E V I -

1141 CCTCGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCAC 1200  
L E K W Q K K K I A E M G P V Q W L A T -

1201 TCAAAAGAAGGCAGCAGACAAAGTCGTCTTCTTCTTCCAATGACGTCAACAGTGTGTG 1260  
Q K K A A D K V V F L L S N D V N S V C -

1261 CGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCC 1320  
D G T C G K S E G S P S E N S Q D L F P -

1321 CCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGT 1440  
L A F N L F C S D L R S Q I H L H K Y V -

1441 GGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCC 1500  
V V Y F R E I D T K D D Y N A L S V C P -

1501 CAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCA 1560  
K Y H L M K D A T A F C A E L L H V K Q -

1561 GCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCC 1620  
Q V S A G K R S Q A C H D G C C S L \*

1621 CACCCATGAGAAGCAAGAGACCTTAAAGGCTTCTATCCCACCAATTACAGGGAAAAAAC 1680

1681 GTGTGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAACATTT 1740

1741 TATACCAATAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAAC 1800

1801 TACATTTACAACCTTCAAAGCTGTTTTATACATAGAAAATCAATTACAGCTTTAATTGAAAA 1860

1861 CTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCAGC 1901

**FIGURE 2**  
Homology of a First IL-17 human Receptor Like Polypeptide  
Amino Acid Segeunce (SEQ ID NO: 2) and Known Human IL-17  
Receptor Family Member (SEQ ID NO: 3)

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1 .....MSLVLLSLAALCRSAVPREP 20
      || || || |
1 MGAARSPPSAVPGPLLGLLLLLLGV LAPGGASLRLLDHRALVCSQPGLNC 50
21 TVQCGSETGPSPEWMLQHDLP GDRLRLRVEPVTTSVATGDYSILMNVS 70
      || . . | . . | | : || : : || . . : |
51 TVK..NSTCLDDSWIHPRNLTPSSPKDLQIQLFHAHTQQGDLFPVAHIEW 98
71 VLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWT 120
      | . |||| | . : | . | || | . . | : |
99 TLQTDASILYLEGAELSVLQLNTNERLCVRFE....FLSKLRHHHRRWR 143
121 FSYIGFPPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYK 170
      | : | | : . | : | : | . | | | | | | |
144 FTFSHFVVDPDQYEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVT 193
171 KKC VKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QH 213
      | . . ||||| | | . | . | | | | : |
194 TPCMSSGSLWDPNITVETLEAHQLRVSF TLWNETHYQILLTSFPHMENH 243
214 STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSD 260
      | : | : | . . . | | . . | | : | : | . |
244 SCFEHMHHIPAPRPEEFHQRSNVTLT LRLNLKGCCR HQVQIQPFSSCLND 293
261 CIRHKGTVVLCPO.TGVFPPLDNNKSKPGGWLPLLLLSLLVATWVLVAGI 309
      | : || | | || : | | : . | : : | : | . | : :
294 CLRHSAT.VSCPEMPDTPEPIPDY MPLWVYWF.ITGISILLVGSVILLIV 341
310 YLMWRHERIKKTSFSTTT.....LLP....PIKVLVVYPSE.ICF 344
      : || : | : | | : | | | | : | : | :
342 CMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLY 391
345 HHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK....KAAD 390
      : | : || | . || | : : . | . | . | |
392 VDVVLKFAQFLLTACGTEVALDLL EEQATSEAGVMTWVGRQKQEMVESNS 441
391 KVVFLLSNDVNSVCDGTCGKSEGSP.....SENSQDLFPLAFNLFCS 433
      | : : | | . | : | . | | | | | : |
442 KIIVLC SRGTRAKWQALLGR..GAPVRLRCDHGKPVGD LFTAAMNMILPD 489
481 LRSQIHLHKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELL 480
      : | | | | | : | . | : | | : | : |
490 FKR PACFGTYVVCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDL 539
481 HVKQQVSAGKRSQACHDGCCSL*..... 503
      . | : : |
540 EMFQPGRMHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECEN 589

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FIGURE 3A  
Map of a Second Human IL-17 Receptor Like cDNA (SEQ ID NO: 4)  
And Amino Acid (SEQ ID NO: 5) Sequences

1 ATAAAGCGC AGCGTGCGGGTG GCCTGGATCCCG CGCAGTGGCCCG GCGATGTCGCTCGT 60  
M S L V -  
61 GCTGCTAAG CCTGGCCGCGCT GTGCAGGAGCGC CGTACCCCGAGAGCCGACCGTTCAATG 120  
L L S L A A L C R S A V P R E P T V Q C -  
121 TGGCTCTGA AACTGGGCCATC TCCAGAGTGGAT GCTACAACATGA TCTAATCCCCGGA 180  
G S E T G P S P E W M L Q H D L I P G D -  
181 CTTGAGGGA CCTCCGAGTAGA ACCTGTTACAAC TAGTGTTGCAAC AGGGGACTATTC AAT 240  
L R D L R V E P V T T S V A T G D Y S I -  
241 TTTGATGAA TGTAAGCTGGGT ACTCCGGGCAGA TGCCAGCATCCG CTGTTGAAGGC CAC 300  
L M N V S W V L R A D A S I R L L K A T -  
301 CAAGATTTG TGTGACGGGCAA AAGCAACTTCCA GTCCTACAGCTG TGTGAGGCTGGAGTG 360  
K I C V T G K S N F Q S Y S C V R L E C -  
361 CAGTGGTGC GATCATGGCTCG CTGCGACCTCAA TCTTCTGGGCTC AAGCGATCGTTC TGC 420  
S G A I M A R C D L N L L G S S D R S A -  
421 TTCAGCCTC CCGAGCGGCTGG GACTGCAGGCGT GGGCCACCAGAC CTGGCTAATTTT TGT 480  
S A S R A A G T A G V G H Q T W L I F V -  
481 AGTTTTTGT AGAGGGGGGTTT CACCGTGTGCT GGTCTTGAATTC CAGTGCTCAGGC GAT 540  
V F V E G G F T V L L V L N S S A Q A I -  
541 CTGCCTGCC TCGGCTTCCCAA AGTGCTGGGATT ACAGTGGACATT TTCCTACATCGG CTT 600  
C L P R L P K V L G L Q W T F S Y I G F -  
601 CCCTGTAGA GCTGAACACAGT CTATTTTATTGG GGCCATAATAT TCCTAATGCAAA TAT 660  
P V E L N T V Y F I G A H N I P N A N M -  
661 GAATGAAGA TGGCCCTTCCAT GTCTGTGAATTT CACCTCACCAGG CTGCCTAGACCA CAT 720  
N E D G P S M S V N F T S P G C L D H I -  
721 AATGAAATA TAAAAAAAGTG TGTCAAGGCCGG AAGCCTGTGGGA TCCGAACATCACT TGC 780  
M K Y K K K C V K A G S L W D P N I T A -  
781 TTGTAAGAA GAATGAGGAGAC AGTAGAAGTGAA CTTCAACAACCAC TCCCCTGGGAAA CAG 840  
C K K N E E T V E V N F T T T P L G N R -  
841 ATACATGGC TCTTATCCAACA CAGCACTATCAT CGGGTTTCTCA GGTGTTTGA GCCACA 900  
Y M A L I Q H S T I I G F S Q V F E P H -  
901 CCAGAAGAA ACAAACGCGAGC TTCAGTGGTGAT TCCAGTGACTGG GGATAGTGAAGG TGC 960  
Q K K Q T R A S V V I P V T G D S E G A -  
961 TACGGTGCA GCTGACTCCATA TTTTCTACTTGT TGGCAGCGACTG CATCCGACATAA AGG 1020  
T V Q L T P Y F P T C G S D C I R H K G -

Figure 3B

1021 AACAGTTGT GCTCTGCCCACA AACAGGCGTCCC TTTCCCTCTGGA TAACAACAAAAG CAA 1080  
T V V L C P Q T G V P F P L D N N K S K -

1081 GCCGGGAGG CTGGCTGCCTCT CCTCCTGCTGTC TCTGCTGGTGGC CACATGGGTGCT GGT 1140  
P G G W L P L L L L S L L V A T W V L V -

1141 GGCAGGGAT CTATCTAATGTG GAGGCACGAAAG GATCAAGAAGAC TTCCTTTTCTAC CAC 1200  
A G I Y L M W R H E R I K K T S F S T T -

1201 CACACTACT GCCCCCATTAA GGTTCTTGTGGT TTACCCATCTGA AATATGTTTCCA TCA 1260  
T L L P P I K V L V V Y P S E I C F H H -

1261 CACAATTTG TTA CTTC TACTGA ATTTCTTCAAAA CCATTGCAGAAG TGAGGTCATCCT CGA 1320  
T I C Y F T E F L Q N H C R S E V I L E -

1321 AAAGTGGCA GAAAAAGAAAAT AGCAGAGATGGG TCCAGTGCAGTG GCTTGCCACTCA AAA 1380  
K W Q K K K I A E M G P V Q W L A T Q K -

1381 GAAGGCAGC AGACAAAGTCGT CTTCTTCTTTT CAATGACGTCAA CAGTGTGTGCGA TGG 1440  
K A A D K V V F L L S N D V N S V C D G -

1441 TACCTGTGG CAAGAGCGAGGG CAGTCCCAGTGA GAACTCTCAAGA CCTCTTCCCCCT TGC 1500  
T C G K S E G S P S E N S Q D L F P L A -

1501 CTTTAACCT TTTCTG CAGTGA TCTAAGAAGCCA GATTCACTGCA CAAATACGTGGT GGT 1560  
F N L F C S D L R S Q I H L H K Y V V V -

1561 CTACTTTAG AGAGATTGATAC AAAAGACGATTA CAATGCTCTCAG TGTCTGCCCCAA GTA 1620  
Y F R E I D T K D D Y N A L S V C P K Y -

1621 CCACCTCAT GAAGGATGCCAC TGCTTTCTGTGC AGAACTTCTCCA TGTCAAGCAGCA GGT 1680  
H L M K D A T A F C A E L L H V K Q Q V -

1681 GTCAGCAGG AAAAAGATCACA AGCCTGCCACGA TGGCTGCTGCTC CTTGTAGCCCAC CCA 1740  
S A G K R S Q A C H D G C C S L \*

1741 TGAGAAGCA AGAGACCTTAAA GGCTTCCTATCC CACCAATTACAG GGAAAAACGTG TGA 1800

1801 TGATCCTGA AGCTTACTATGC AGCCTACAAACA GCCTTAGTAATT AAAACATTTTAT ACC 1860

1861 AATAAAATT TTCAAATATTGC TAACTAATGTAG CATTA ACTAACG ATTGGAACTAC ATT 1920

1921 TACAAC TTC AAAGCTGTTTTA TACATAGAAATC AATTACAGCTTT AATTGAAA ACTG TAA 1980

1981 CCATTTTGA TAATGCAACAAT AAAGCATCTTCAG C 2015

FIGURE 4  
Homology of a Second IL-17 Human Receptor Like Polypeptide  
Amino Acid Sequence (SEQ ID No: 5) and Known Human IL 17  
Receptor Family Mamber (SEQ ID NO: 3)

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1 MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRV 50
1 .....MGAARS 6
51 EPVTTSVATGDYSILMNVSIVLR.ADASIRLL.KATKICVTGKSNFQSYS 98
7 PP..SAVPGPILLGLLLLLLGLVAPGGASLRLLDHRALVCSQPGLNCTVKN 54
99 CVRLECSGAIMARCDLNLGSSDRSA.....SASRAAGTAGVGHQNWLI 142
55 STCLDDSW.IHPR...NLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL 100
143 ....FVVFVEGGFTVLLVLNSSAQAICL..PRLPKVL..GLQWTFYSYIGF 184
101 QTDASILYLEGAELSVLQLNTN.ERLCVRFEFLSKLRHHHRRWRFTFSHF 149
185 PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKA 234
150 VVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
235 GSLWDPNITACKNEETVEVNFTTTPLGNRYMALI.....QHSTIIGF 277
200 GSLWDPNITVETLEAHQLRVSF TLWNETHYQILLTSFPHMENHSCFEHM 249
278 SQVFEPHQKKQTRASVVIPTVGDSEGA...TVQLTPYFPTCGSDCIRHKG 324
250 HHIPAPRPPEEFHQRSNVTTLTLNLKGCCRHQVQIQPFSSCLNDCLRHS 299
325 TVVLCPQ.TGVPFPLDNNKSKPGGWLPLLLLLSLLVATWVLVAGIYLMWRH 373
300 T.VSCPEMPDTPEPIPDYMLVWYWF.ITGISILLVGSVILLIVCMTWRL 347
374 ERIKTSFSTTT.....LLP...PIKVLVVYPSE.ICFHHTICY 408
348 AGPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLYVDVVLK 397
409 FTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK...KAADKVVFLL 454
398 FAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLC 447
455 SNDVNSVCDGTGCGKSEKSP.....SENSQDLFPLAFNLFCSDLRSQIH 497
448 SRGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPAC 495
498 LHKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELLHVKKQV 544
496 FGTYVVVYFSEVSCDGDVPLDGAAPRYPLMDRFEEVYFRIQDLEMFQPG 545
545 SAGKRSQACHDGCCSL*..... 561
546 RMHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECENLYSADD 595

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FIGURE 5A  
Map of a Third IL-17 Receptor Like cDNA (SEQ ID NO: 6)  
and Amino Acid (SEQ ID NO: 7) Sequence

1 ATAAAAGCGCAGCGTGC GGGTGGCCTGGATCCCGCGCAGTGGCCCGGCGATGTCGCTCGT 60  
61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120  
121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCGGGAGA 180  
181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTGCAACAGGGGACTATTCAAT 240  
241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGTGGACATTTTCCTACATCGGCTTCC 300  
M W T F S Y I G F P -  
301 CTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCAT AATATTCCTAATGCAAATATGA 360  
V E L N T V Y F I G A H N I P N A N M N -  
361 ATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAA 420  
E D G P S M S V N F T S P G C L D H I M -  
421 TGAAATATAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTT 480  
K Y K K K C V K A G S L W D P N I T A C -  
481 GTAAGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAACCACTCCCCTGGGAAACAGAT 540  
K K N E E T V E V N F T T T P L G N R Y -  
541 ACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACC 600  
M A L I Q H S T I I G F S Q V F E P H Q -  
601 AGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTA 660  
K K Q T R A S V V I P V T G D S E G A T -  
661 CGGTGCAGCTGACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAA 720  
V Q L T P Y F P T C G S D C I R H K G T -  
721 CAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTTCCCTCTGGATAACAACAAAAGCAAGC 780  
V V L C P Q T G V P F P L D N N K S K P -  
781 CGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGG 840  
G G W L P L L L L S L L V A T W V L V A -  
841 CAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCA 900  
G I Y L M W R H E R I K K T S F S T T T -  
901 CACTACTGCCCCCATTAAAGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACA 960  
L L P P I K V L V V Y P S E I C F H H T -  
961 CAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTCGAAA 1020  
I C Y F T E F L Q N H C R S E V I L E K -  
1021 AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAAGA 1080  
W Q K K K I A E M G P V Q W L A T Q K K -  
1081 AGGCAGCAGACAAAGTCGTCTTCTCTTTTCCAATGACGTCAACAGTGTGTGCGATGGTA 1140  
A A D K V V F L L S N D V N S V C D G T -  
1141 CCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCT 1200  
C G K S E G S P S E N S Q D L F P L A F -

Figure 5B

1201 TTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGTCT 1260  
N L F C S D L R S Q I H L H K Y V V V Y -  
1261 ACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACC 1320  
F R E I D T K D D Y N A L S V C P K Y H -  
1321 ACCTCATGAAGGATGCCACTGCTTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGT 1380  
L M K D A T A F C A E L L H V K Q Q V S -  
1381 CAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCCCACCCATG 1440  
A G K R S Q A C H D G C C S L \*  
1441 AGAAGCAAGAGACCTTAAAGGCTTCCATCCCACCAATTACAGGGAAAAAACGTGTGATG 1500  
1501 ATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAACATTTTATACCAA 1560  
1561 TAAATTTTCAAATATTGCTAACTAATGTAGCATTAACCTAACGATTGGAACTACATTTA 1620  
1621 CAACTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAAGTGTAAACC 1680  
1681 ATTTTGATAATGCAACAATAAAGCATCTTCAGC 1713





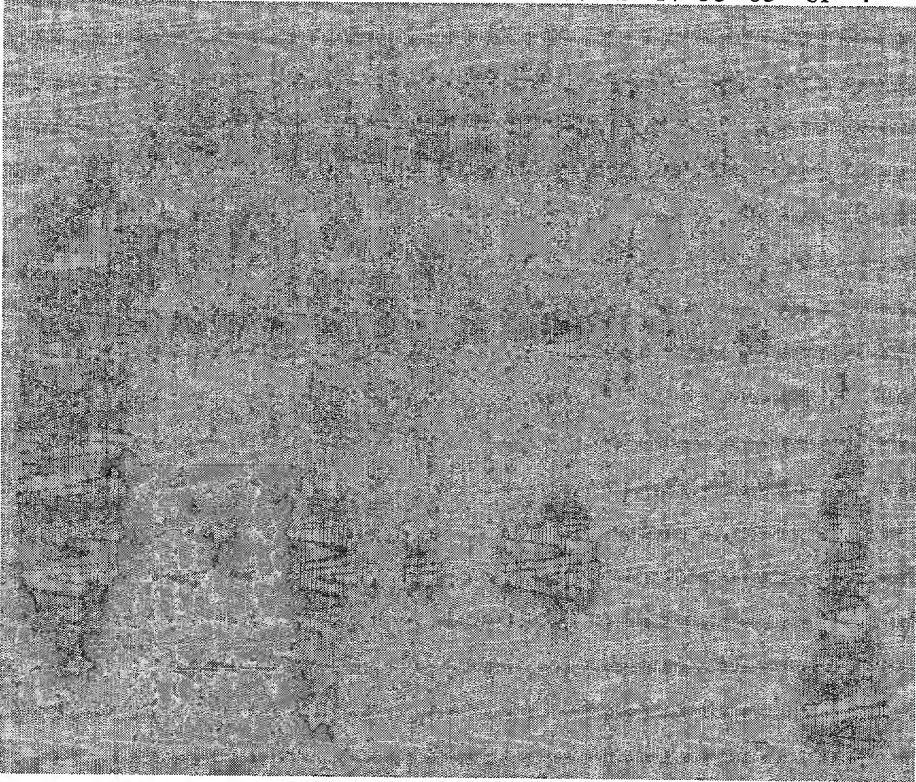
FIGURE 7  
Overlap of Amino Acid Sequences of the First (SEQ ID NO: 2),  
Second (SEQ ID NO: 5), and Third (SEQ ID NO: 7) Human IL-17  
Receptor Like Polypeptides

1	<b>MSLVLLS LAA</b>	<b>LCRS</b>	AVPREP	TVQCGSETG P	SPEWMLQHDL	IPGDLRDLRV
1	<b>MSLVLLS LAA</b>	<b>LCRS</b>	AVPREP	TVQCGSETG P	SPEWMLQHDL	IPGDLRDLRV
51	EPVTTSVATG	DYSILMNV SW	VL	RADASIRL	LKATKICVTG	KSNFQSYSCV
51	EPVTTSVATG	DYSILMNV SW	VL	RADASIRL	LKATKICVTG	KSNFQSYSCV
101	RCNYTEAFQT	QTRPSGGK --	-----	-----	-----	-----
101	RLECSGAIMA	RCDLNLG SS	DRSASASRAA	GTAGVGHQNW	LIFVVVFVEGG	
119	-----	-----	-----	WTF S	YIGFPVELNT	VYFIGAHNIP
151	FTVLLVLNSS	AQAICLPRLP	KVLGLQWTF S	YIGFPVELNT	VYFIGAHNIP	
1			MWTF S	YIGFPVELNT	VYFIGAHNIP	
143	NANMNED GPS	MSVNFTSP GC	LDHIMKYKK K	CVKAGSLWDP	NITACKKNEE	
201	NANMNED GPS	MSVNFTSP GC	LDHIMKYKK K	CVKAGSLWDP	NITACKKNEE	
26	NANMNED GPS	MSVNFTSP GC	LDHIMKYKK K	CVKAGSLWDP	NITACKKNEE	
193	TVEVNFT TTP	LGNRYMAL IQ	HSTIIGFSQ V	FEPHQKKQTR	ASVVIPVTGD	
251	TVEVNFT TTP	LGNRYMAL IQ	HSTIIGFSQ V	FEPHQKKQTR	ASVVIPVTGD	
76	TVEVNFT TTP	LGNRYMAL IQ	HSTIIGFSQ V	FEPHQKKQTR	ASVVIPVTGD	
243	SEGATVQLTP	YFPTCGSD CI	RHKGTVVLC P	QTGVPFPLDN	NKSKPGGWLP	
301	SEGATVQLTP	YFPTCGSD CI	RHKGTVVLC P	QTGVPFPLDN	NKSKPGGWLP	
126	SEGATVQLTP	YFPTCGSD CI	RHKGTVVLC P	QTGVPFPLDN	NKSKPGGWLP	
293	<u>LLLLSLL VAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>	
351	<u>LLLLSLL VAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>	
176	<u>LLLLSLL VAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>	
343	CFHHTICYFT	EFLQNHCR SE	VILEKWQKK K	IAEMGPVQWL	ATQKKAADKV	
401	CFHHTICYFT	EFLQNHCR SE	VILEKWQKK K	IAEMGPVQWL	ATQKKAADKV	
226	CFHHTICYFT	EFLQNHCR SE	VILEKWQKK K	IAEMGPVQWL	ATQKKAADKV	
393	VFLLSND VNS	VCDGTCGK SE	GSPSENSQD L	FPLAFNLFCS	DLRSQIHLHK	
451	VFLLSND VNS	VCDGTCGK SE	GSPSENSQD L	FPLAFNLFCS	DLRSQIHLHK	
276	VFLLSND VNS	VCDGTCGK SE	GSPSENSQD L	FPLAFNLFCS	DLRSQIHLHK	
443	YVVVYFREID	TKDDYNAL SV	CPKYHLMKD A	TAFCAELLHV	KQQVSAGKRS	
501	YVVVYFREID	TKDDYNAL SV	CPKYHLMKD A	TAFCAELLHV	KQQVSAGKRS	
326	YVVVYFREID	TKDDYNAL SV	CPKYHLMKD A	TAFCAELLHV	KQQVSAGKRS	
493	QACHDGC CSL	*				
551	QACHDGC CSL	*				
376	QACHDGC CSL	*				

Figure 8

Northern Blot Expression Analysis of TH00-018  
Necropsied Transgenic Founders

	Transgenics								control						
M	1	16	27	29	55	61	20	52	66	2	17	53	65	bl	+



0.54 kb →

Figure 9

Northern Blot Expression Analysis of TH00-018  
Hepatectomized Transgenic Founders

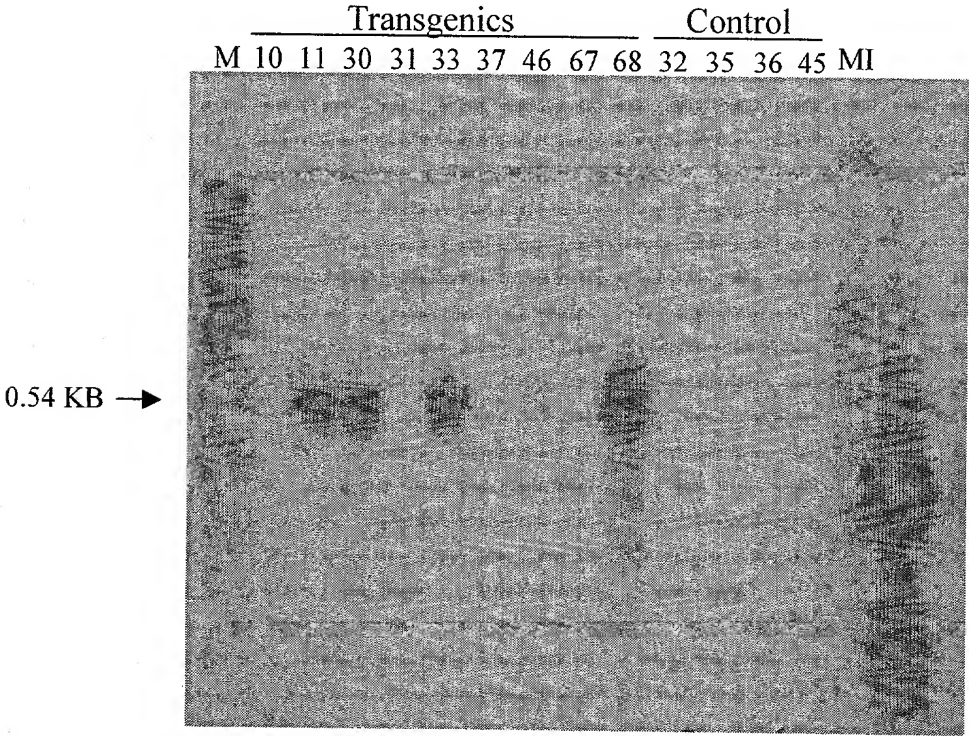


Figure 10

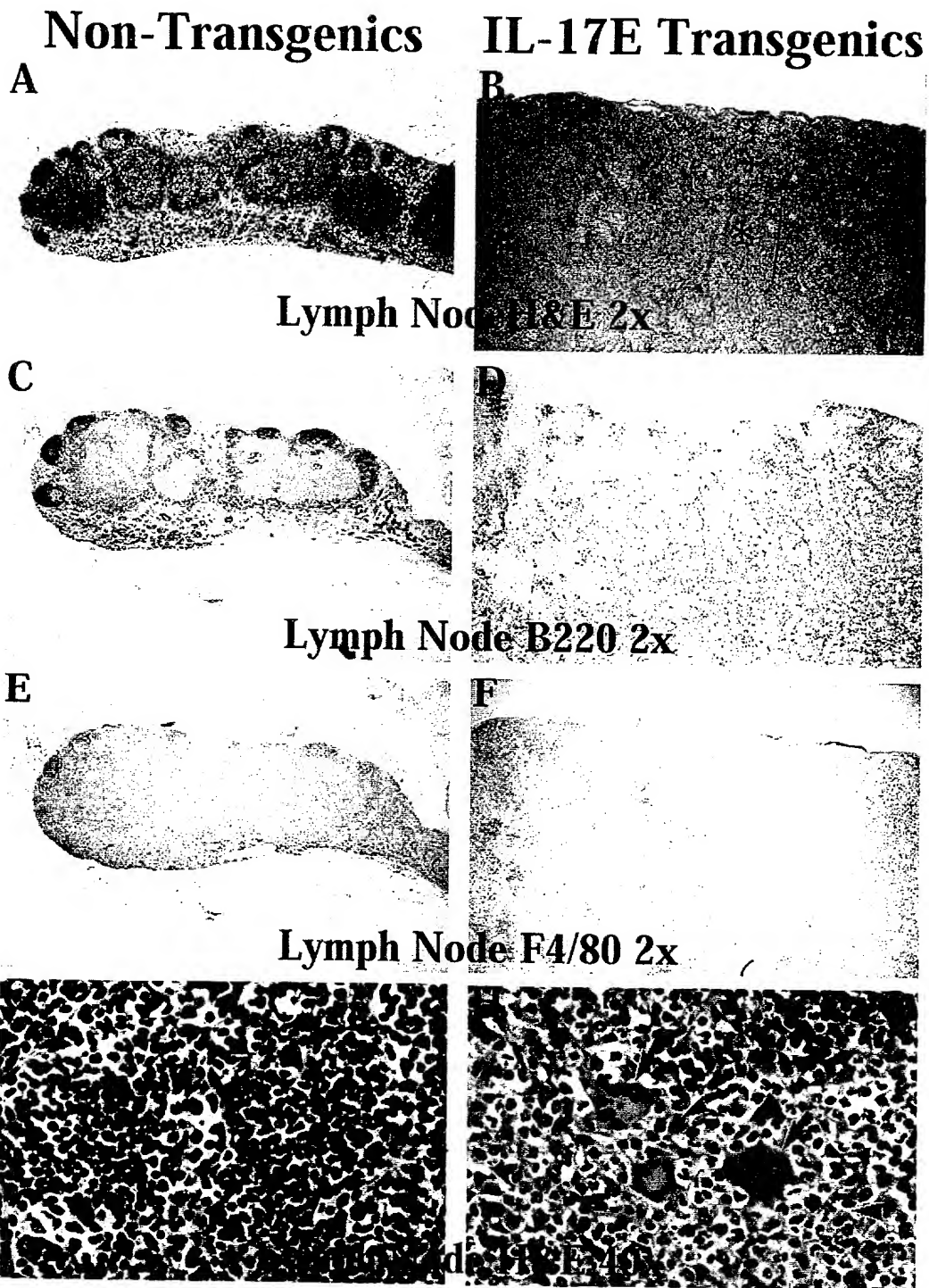


Figure 11

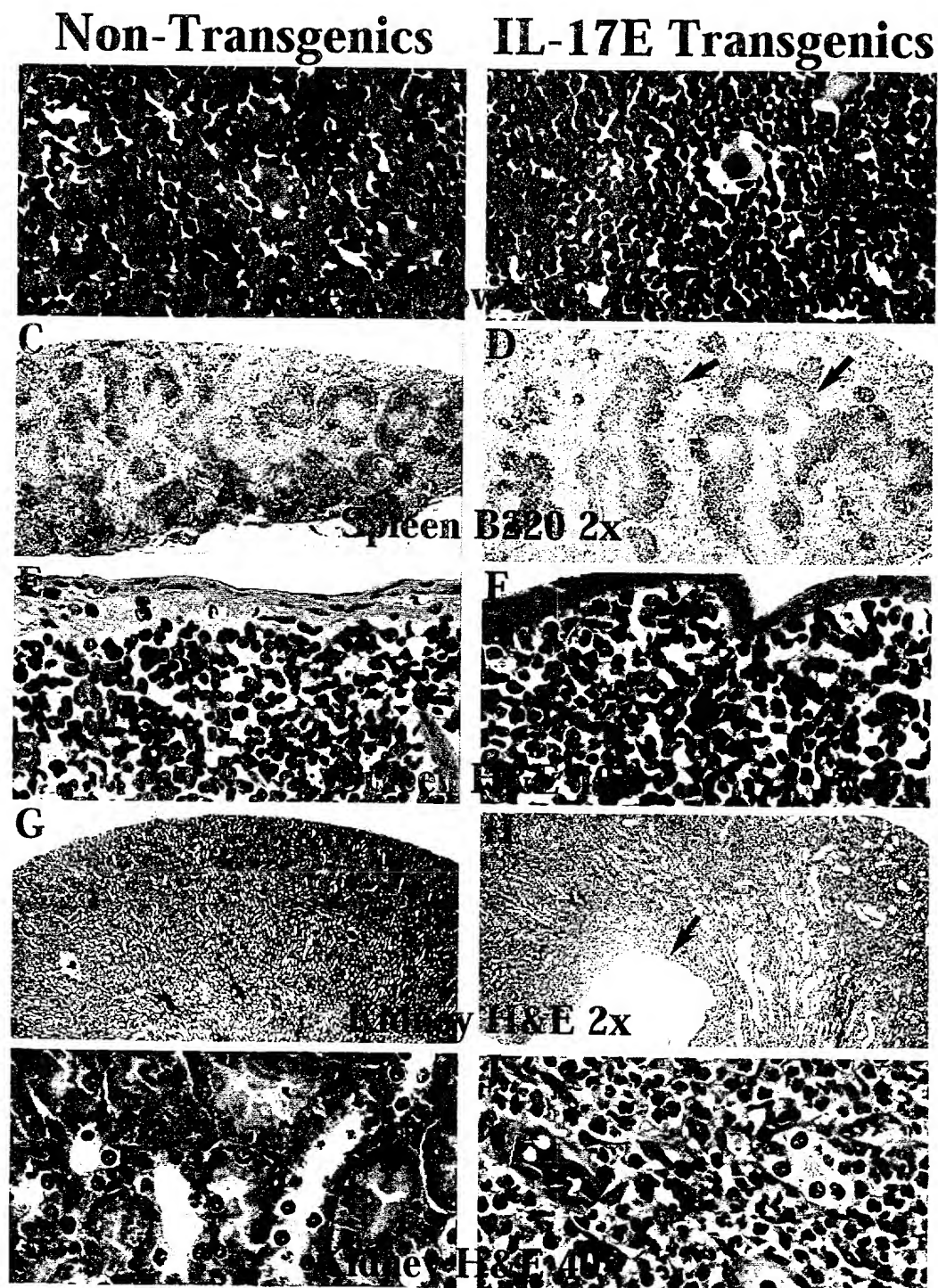


Figure 12

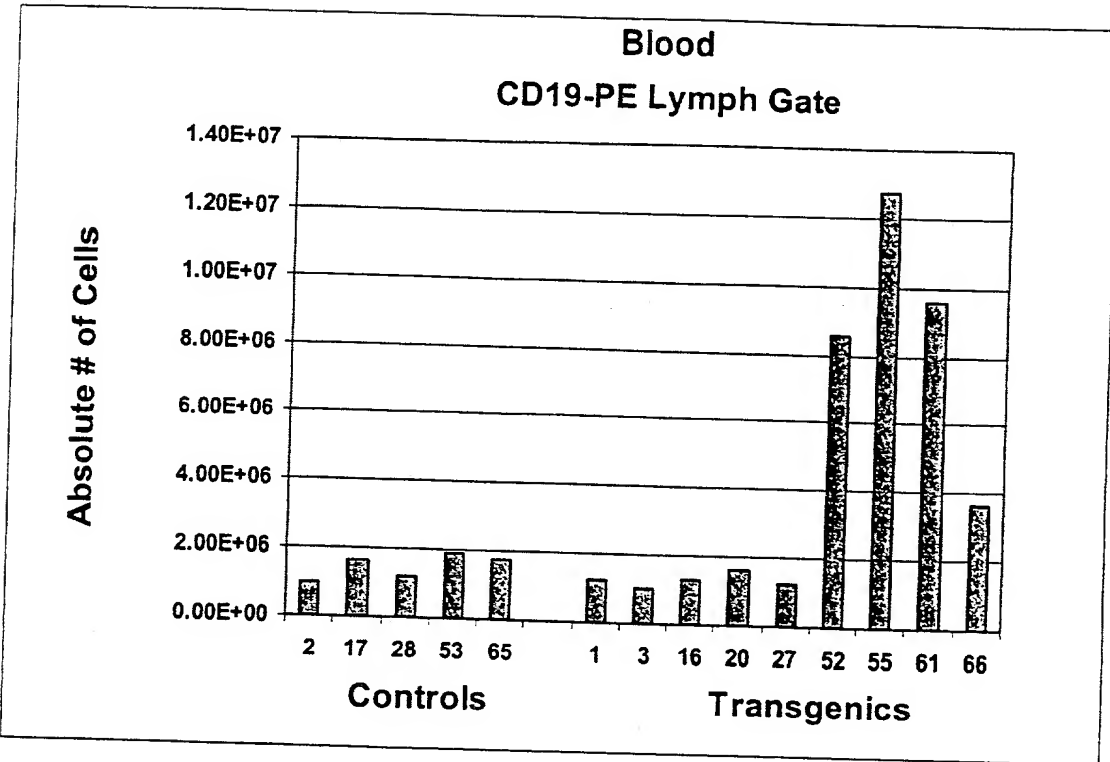


Figure 13

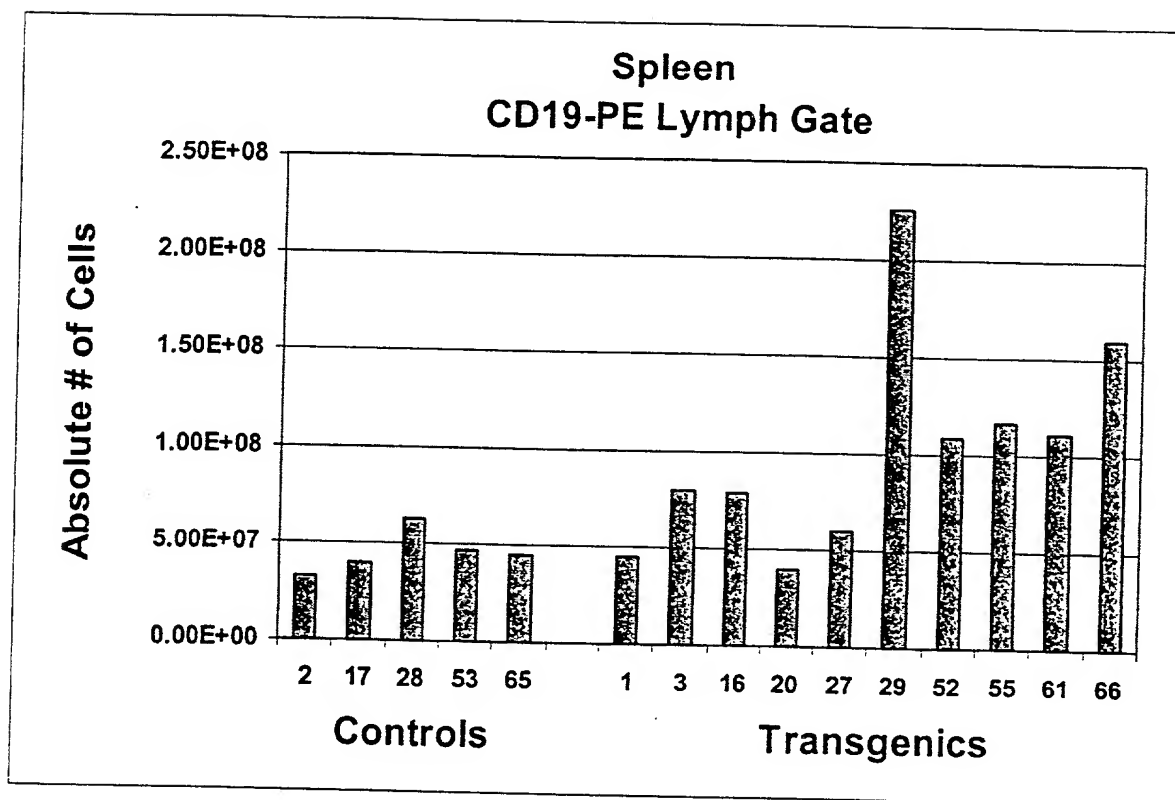




Figure 14

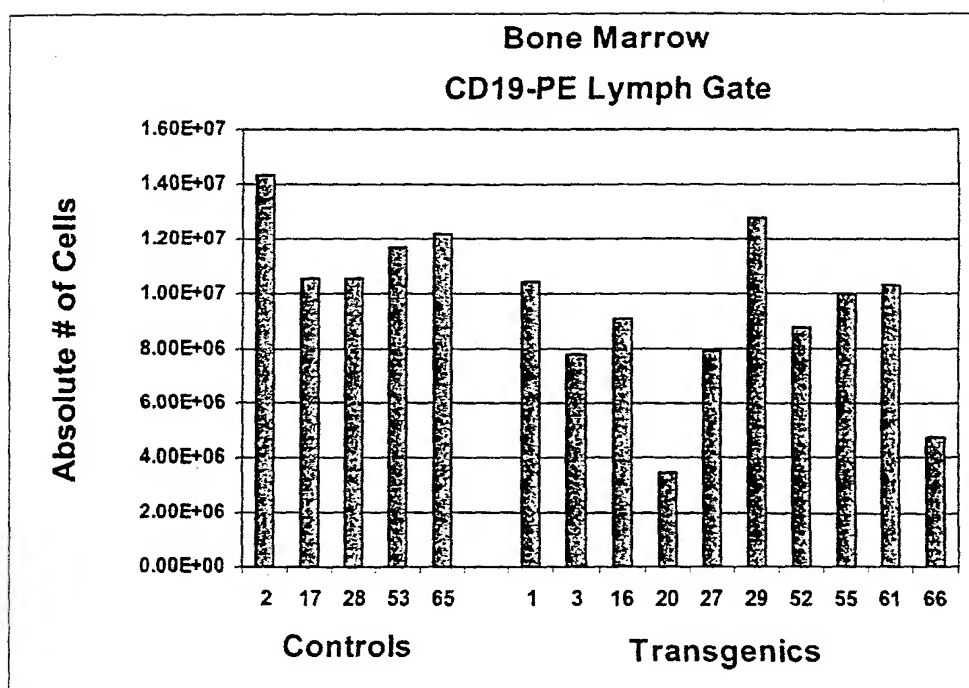


Figure 15

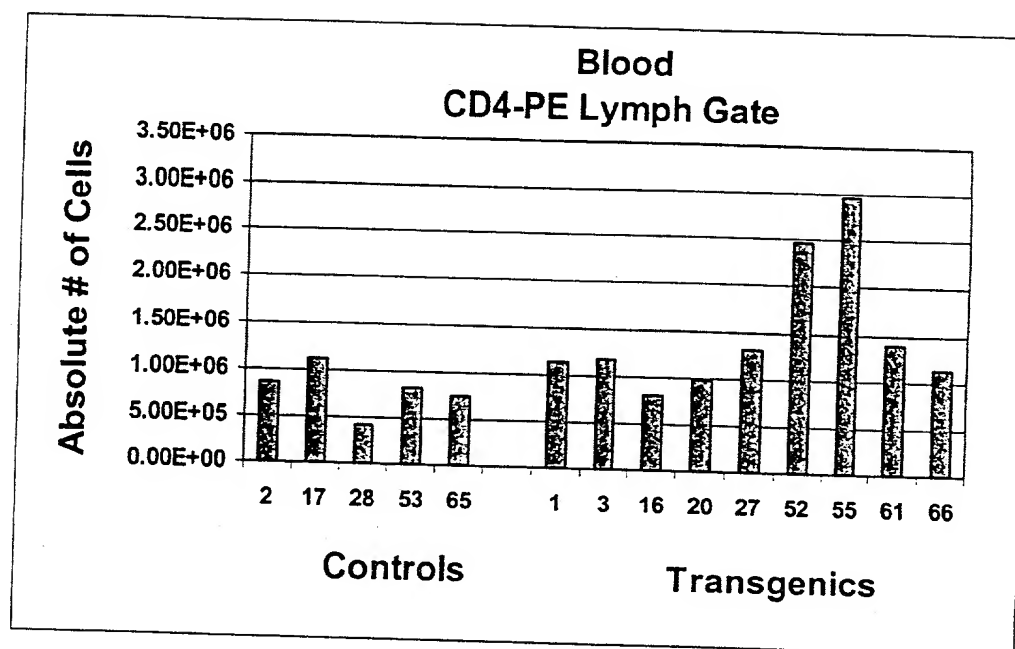


Figure 16

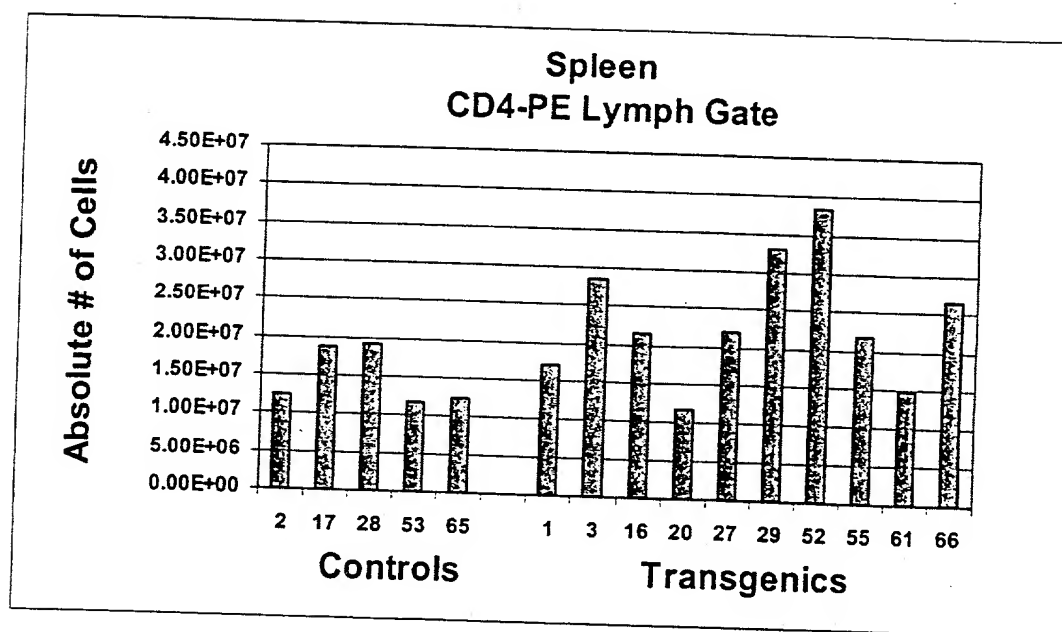
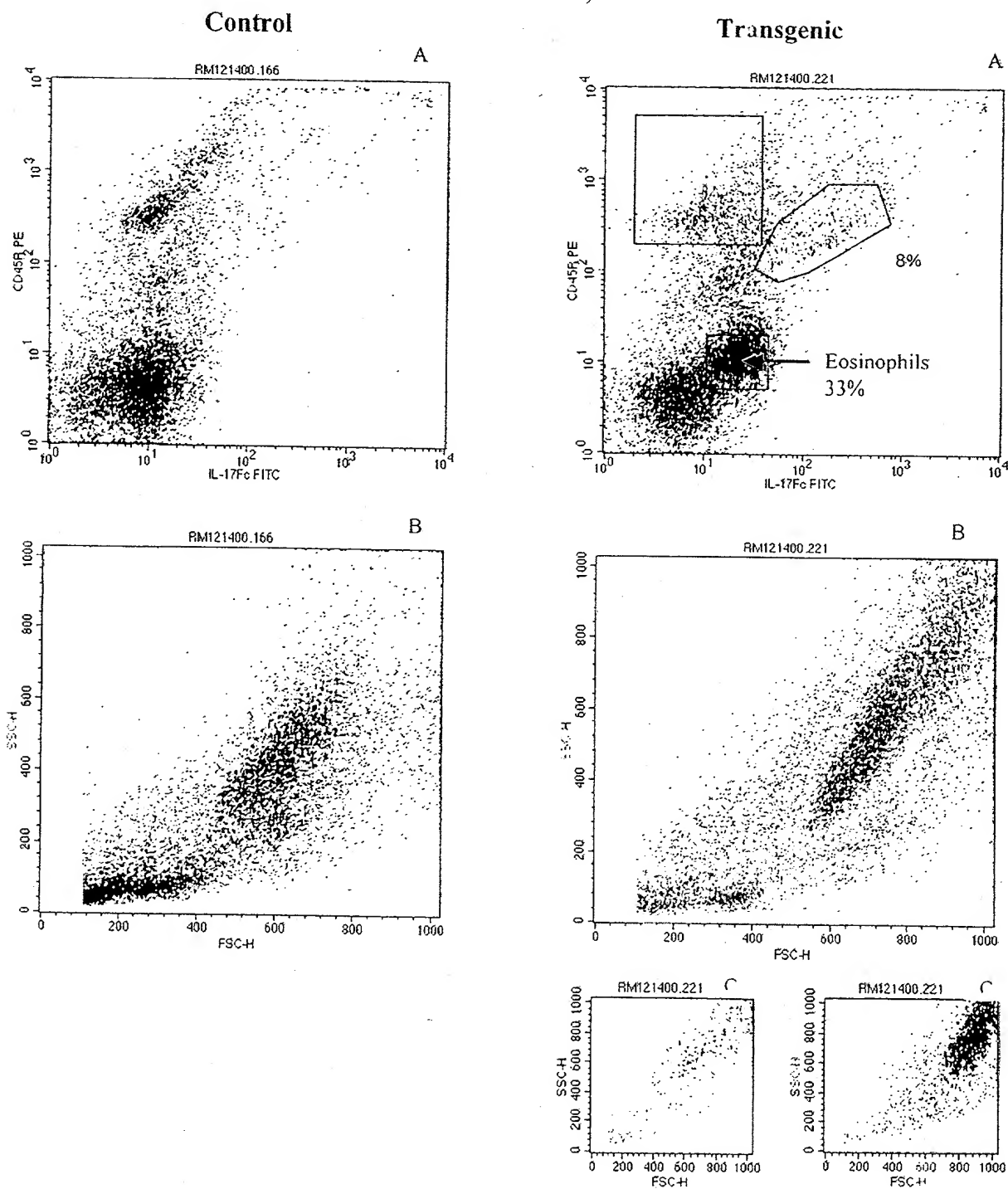


Figure 17

# CD45R+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW



Granulocyte-like  
cells

Eosinophil-like cells

Figure 18

# CD4+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW

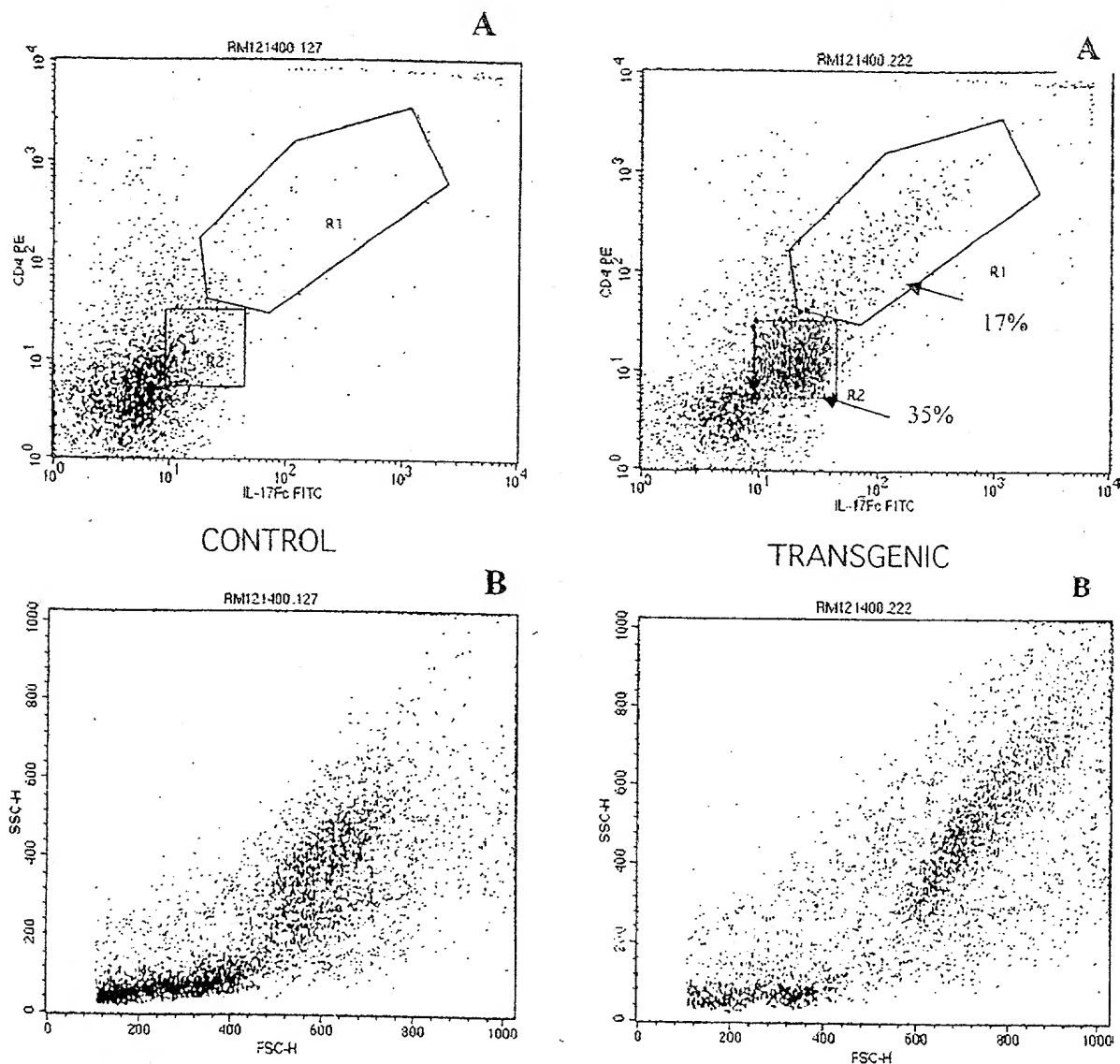


Figure 21

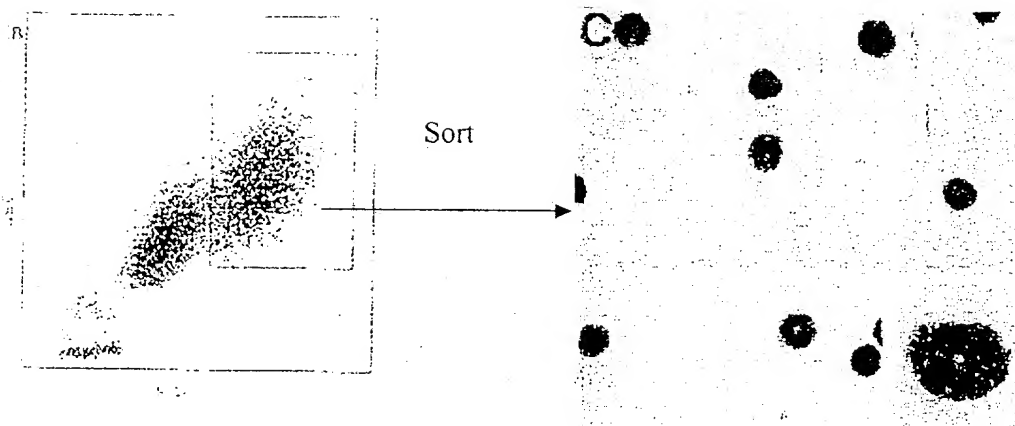


Figure 19

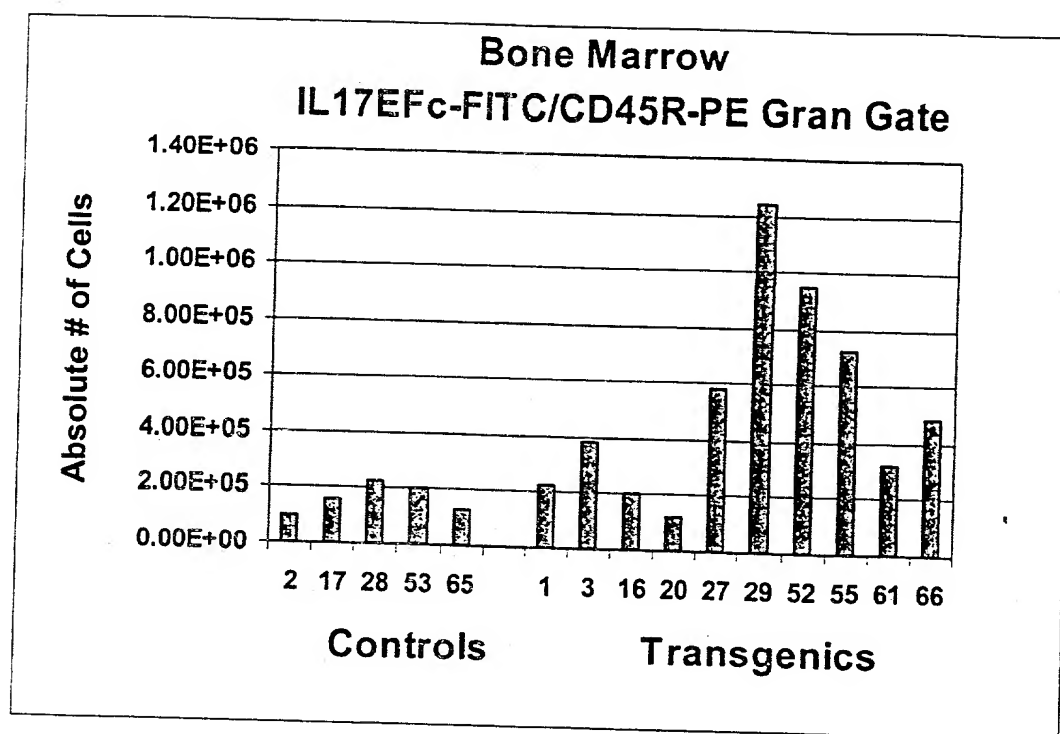


Figure 20

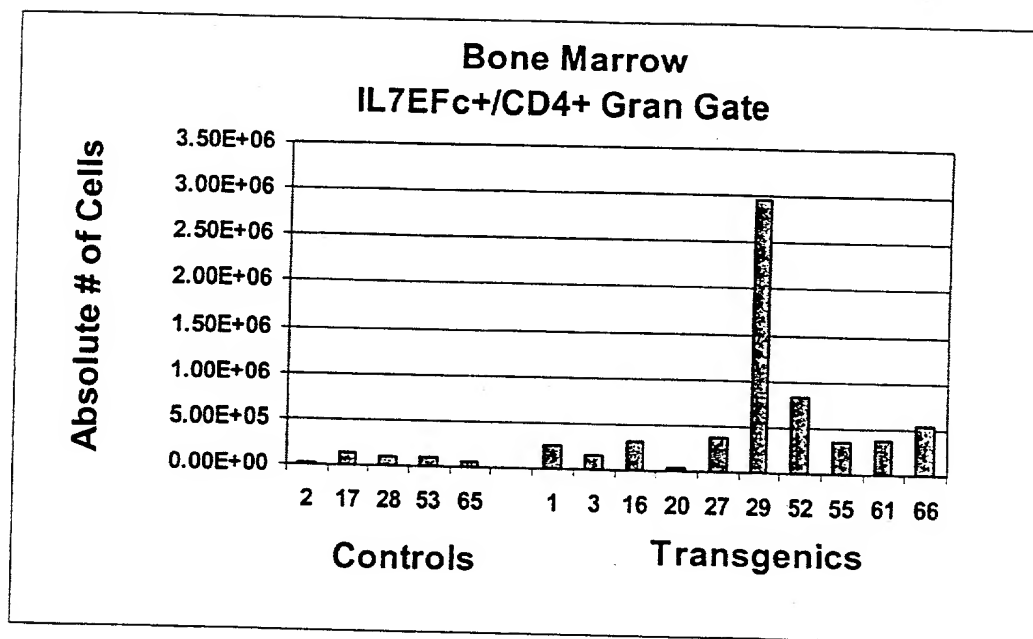




Figure 22

IL-17RB-2 Fusion Protein (SEQ ID NO: 24)

1     **MSLVLLSLAA** **LCRS**AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV  
51    EPVTTSVATG DYSILMNVS **W** VLRADASIRL LKATKICVTG KSNFQSYSCV  
101   RCNYTEAFQT QTRPSGGKWT FSYIGFPVEL NTVYFIGAHN IPNANMNEDG  
151   PSMSVNFTSP GCLDHIMKYK KKC**V**KAGSLW DPNITACKKN EETVEVNFTT  
201   TPLGNRYMAL IQHSTIIGFS QVFEPHQKKQ TRASVVIPVT GDSEGATVQL  
251   TPYFPTCGSD CIRHKGT**V**VL CPQTGV**P**PL DNNKSKPGGW LPAAAE**P**KSC  
301   DKTHTCPPCP APELLGGPSV FLFP**P**KPKDT LMISRTPEVT CVVVDV**S**HED  
351   PEVKFNWYVD GVEVHNA**K**TK PREEQYNSTY RVVSVLTVLH QDWLNGKEY**K**  
401   CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLTCLV**K**  
451   GFYPSDIAVE WESNGQ**P**ENN YKTPPVLD**S** DGSFFLYSKL TVDKSRWQ**Q**G  
501   NVFSCSVMHE ALHNHYTQKS LSLSPG**K**\*

Figure 23

Fusion Protein for IL-17RB-3 (SEQ ID NO: 25)

1    **MSLVLLSLAA** **LCRS**AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV  
51    EPVTTSVATG DYSILMNVS W VLRADASIRL LKATKICVTG KSNFQSYSCV  
101   RLECSGAIMA RCDLNLLGSS DRSASASRAA GTAGVGHQTW LIFVVFVEGG  
151   FTVLLVLNSS AQAICLPRLP KVLGLQWTFS YIGFPVELNT VYFIGAHNIP  
201   NANMNEDGPS MSVNFTSPGC LDHIMKYKKK CVKAGSLWDP NITACKKNEE  
251   TVEVNFTTTP LGNRYMALIQ HSTIIGFSQV FEPHQKKQTR ASVVIPVTGD  
301   SEGATVQLTP YFPTCGSDCI RHKGTVVLCP QTGVFPPLDN NKSKPGGWLP  
351   **AAAE**PKSCDK **THTC**PPCPAP **ELLG**GPSVFL **FPPK**PKDTLM **ISRT**PEVTCV  
401   **VVDV**SHEDPE **VKFN**WYVDGV **EVHN**AKTKPR **EEQY**NSTYRV **VSVL**TVLHQD  
451   **WLNG**KEYKCK **VSNK**ALPAPI **EKTIS**KAKGQ **PREP**QVYTL P**SRDEL**TKNQ  
501   **VSLT**CCLKGF **YPSD**IAVEWE **SNGQ**PENNYK **TTPP**VLDSDG **SFFLY**SKLTV  
551   **DKSR**WQQGNV **FSCS**VMEAL **HNHY**TQKSLS **LSPG**K\*